

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/530,542
Source: PCT
Date Processed by STIC: 11/21/2005

ENTERED



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/530,542

DATE: 11/21/2005
TIME: 15:49:29

Input Set : A:\1-32724 SEQLIST.TXT
Output Set: N:\CRF4\11212005\J530542.raw

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4 <110> APPLICANT: BAGUTTI; Claudia
5      CHIQUET-EHRISMANN; Ruth
6      DRABIKOWSKI; Krzysztof; Piotr
7      RUBIN-LUCHT; Beatrix; Paulette
9 <120> TITLE OF INVENTION: METHODS FOR DETECTING TENEURIN
10     SIGNALLING AND RELATED SCREENING METHODS
13 <130> FILE REFERENCE: 1-32724A/FMI
15 <140> CURRENT APPLICATION NUMBER: 10/530,542
C--> 16 <141> CURRENT FILING DATE: 2005-04-07
18 <150> PRIOR APPLICATION NUMBER: PCT/EP03/011382
19 <151> PRIOR FILING DATE: 2003-10-14
21 <150> PRIOR APPLICATION NUMBER: GB0223984
22 <151> PRIOR FILING DATE: 2002-10-15
24 <160> NUMBER OF SEQ ID NOS: 20
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 963
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
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34 <221> NAME/KEY: CDS
35 <222> LOCATION: (1)...(963)
36 <223> OTHER INFORMATION: Human teneurin
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41   1           5           10          15
43 cat gaa atg gat cta gct tac acc agt tct tct gat gag agt gaa gat      96
44 His Glu Met Asp Leu Ala Tyr Thr Ser Ser Ser Asp Glu Ser Glu Asp
45   20          25          30
47 gga aga aaa cca aga cag tca tac aac tcc agg gag acc ctg cac gag      144
48 Gly Arg Lys Pro Arg Gln Ser Tyr Asn Ser Arg Glu Thr Leu His Glu
49   35          40          45
51 tat aac cag gag ctg agg atg aat tac aat agc cag agt aga aag agg      192
52 Tyr Asn Gln Glu Leu Arg Met Asn Tyr Asn Ser Gln Ser Arg Lys Arg
53   50          55          60
55 aaa gaa gta gaa aaa tct actcaa gag atg gaa ttc tgt gaa acc tct      240
56 Lys Glu Val Glu Lys Ser Thr Gln Glu Met Glu Phe Cys Glu Thr Ser
57   65          70          75          80
59 cac act ctg tgc tct ggc tac caa aca gac atg cac agc gtt tct cgg      288
60 His Thr Leu Cys Ser Gly Tyr Gln Thr Asp Met His Ser Val Ser Arg
61   85          90          95
63 cat ggc tac cag cta gag atg gga tct gat gtg gac aca gag aca gaa      336

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64 His	Gly	Tyr	Gln	Leu	Glu	Met	Gly	Ser	Asp	Val	Asp	Thr	Glu	Thr	Glu		
65	100				105							110					
67 ggt	gct	gcc	tca	cct	gac	cat	gca	cta	aga	atg	tgg	ata	agg	gga	atg	384	
68 Gly	Ala	Ala	Ser	Pro	Asp	His	Ala	Leu	Arg	Met	Trp	Ile	Arg	Gly	Met		
69	115				120							125					
71 aaa	tca	gag	cat	agt	tcc	tgt	ttg	tcc	agc	cgg	gcc	aac	tct	gca	tta	432	
72 Lys	Ser	Glu	His	Ser	Ser	Cys	Leu	Ser	Ser	Arg	Ala	Asn	Ser	Ala	Leu		
73	130				135						140						
75 tcc	ttg	act	gac	act	gac	cat	gaa	agg	aag	tct	gat	ggg	gaa	aat	gat	480	
76 Ser	Leu	Thr	Asp	Thr	Asp	His	Glu	Arg	Lys	Ser	Asp	Gly	Glu	Asn	Asp		
77 145					150					155			160				
79 gtg	cag	agc	agc	cca	cac	aac	cag	ttc	acc	ttc	aga	ccc	ctc	cca	ccg	528	
80 Val	Gln	Ser	Ser	Pro	His	Asn	Gln	Phe	Thr	Phe	Arg	Pro	Leu	Pro	Pro		
81					165				170			175					
83 cca	cct	ccg	cct	cct	cat	gcc	tgc	acc	tgt	gcc	agg	aag	cca	ccc	cct	576	
84 Pro	Pro	Pro	Pro	Pro	His	Ala	Cys	Thr	Cys	Ala	Arg	Lys	Pro	Pro	Pro		
85					180				185			190					
87 gca	gcg	gac	tct	ctt	cag	agg	aga	tca	atg	act	acc	cgc	agc	cag	ccc	624	
88 Ala	Ala	Asp	Ser	Leu	Gln	Arg	Arg	Ser	Met	Thr	Thr	Arg	Ser	Gln	Pro		
89					195				200			205					
91 agc	cca	gct	gct	cca	gct	ccc	cca	acc	agc	acg	cag	gat	tca	gtc	cat	672	
92 Ser	Pro	Ala	Ala	Pro	Ala	Pro	Pro	Thr	Ser	Thr	Gln	Asp	Ser	Val	His		
93					210				215			220					
95 ctg	cat	aac	agc	tgg	gtc	ctg	aac	agc	aac	ata	cca	ttg	gag	acc	agg	720	
96 Leu	His	Asn	Ser	Trp	Val	Leu	Asn	Ser	Asn	Ile	Pro	Leu	Glu	Thr	Arg		
97 225					230				235			240					
99 cat	ttc	ctg	ttc	aaa	cat	gga	tct	ggt	tcc	tct	gcg	atc	ttc	agt	gca	768	
100 His	Phe	Leu	Phe	Lys	His	Gly	Ser	Gly	Ser	Ser	Ala	Ile	Phe	Ser	Ala		
101					245				250			255					
103 gcc	agt	cag	aac	tac	cct	ctg	aca	tcc	aat	acc	gtg	tac	tcg	ccc	cct	816	
104 Ala	Ser	Gln	Asn	Tyr	Pro	Leu	Thr	Ser	Asn	Thr	Val	Tyr	Ser	Pro	Pro		
105					260				265			270					
107 ccc	agg	cct	cct	cgt	acc	ttt	tcc	cga	cct	gcc	ttt	acc	ttt			864	
108 Pro	Arg	Pro	Leu	Pro	Arg	Ser	Thr	Phe	Ser	Arg	Pro	Ala	Phe	Thr	Phe		
109					275				280			285					
111 aac	aaa	cct	tac	agg	tgc	tgc	aac	tgg	aag	tgc	aca	ttg	agc	gcc		912	
112 Asn	Lys	Pro	Tyr	Arg	Cys	Cys	Asn	Trp	Lys	Cys	Thr	Ala	Leu	Ser	Ala		
113					290				295			300					
115 act	gca	atc	aca	gtg	act	ttg	gcc	ttg	tta	cta	gcc	tat	gtg	att	gca		
116 Thr	Ala	Ile	Thr	Val	Thr	Leu	Ala	Leu	Leu	Leu	Ala	Tyr	Val	Ile	Ala		
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120 Val																	
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126 <212>	TYPE:	PRT															
127 <213>	ORGANISM:	Homo sapiens															
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131 1 5 10 15
132 His Glu Met Asp Leu Ala Tyr Thr Ser Ser Ser Asp Glu Ser Glu Asp
133 20 25 30
134 Gly Arg Lys Pro Arg Gln Ser Tyr Asn Ser Arg Glu Thr Leu His Glu
135 35 40 45
136 Tyr Asn Gln Glu Leu Arg Met Asn Tyr Asn Ser Gln Ser Arg Lys Arg
137 50 55 60
138 Lys Glu Val Glu Lys Ser Thr Gln Glu Met Glu Phe Cys Glu Thr Ser
139 65 70 75 80
140 His Thr Leu Cys Ser Gly Tyr Gln Thr Asp Met His Ser Val Ser Arg
141 85 90 95
142 His Gly Tyr Gln Leu Glu Met Gly Ser Asp Val Asp Thr Glu Thr Glu
143 100 105 110
144 Gly Ala Ala Ser Pro Asp His Ala Leu Arg Met Trp Ile Arg Gly Met
145 115 120 125
146 Lys Ser Glu His Ser Ser Cys Leu Ser Ser Arg Ala Asn Ser Ala Leu
147 130 135 140
148 Ser Leu Thr Asp Thr Asp His Glu Arg Lys Ser Asp Gly Glu Asn Asp
149 145 150 155 160
150 Val Gln Ser Ser Pro His Asn Gln Phe Thr Phe Arg Pro Leu Pro Pro
151 165 170 175
152 Pro Pro Pro Pro His Ala Cys Thr Cys Ala Arg Lys Pro Pro Pro
153 180 185 190
154 Ala Ala Asp Ser Leu Gln Arg Arg Ser Met Thr Thr Arg Ser Gln Pro
155 195 200 205
156 Ser Pro Ala Ala Pro Ala Pro Pro Thr Ser Thr Gln Asp Ser Val His
157 210 215 220
158 Leu His Asn Ser Trp Val Leu Asn Ser Asn Ile Pro Leu Glu Thr Arg
159 225 230 235 240
160 His Phe Leu Phe Lys His Gly Ser Gly Ser Ser Ala Ile Phe Ser Ala
161 245 250 255
162 Ala Ser Gln Asn Tyr Pro Leu Thr Ser Asn Thr Val Tyr Ser Pro Pro
163 260 265 270
164 Pro Arg Pro Leu Pro Arg Ser Thr Phe Ser Arg Pro Ala Phe Thr Phe
165 275 280 285
166 Asn Lys Pro Tyr Arg Cys Cys Asn Trp Lys Cys Thr Ala Leu Ser Ala
167 290 295 300
168 Thr Ala Ile Thr Val Thr Leu Ala Leu Leu Ala Tyr Val Ile Ala
169 305 310 315 320
170 Val
174 <210> SEQ ID NO: 3
175 <211> LENGTH: 1194
176 <212> TYPE: DNA
177 <213> ORGANISM: Homo sapiens
179 <220> FEATURE:
180 <221> NAME/KEY: CDS
181 <222> LOCATION: (1)...(1194)
182 <223> OTHER INFORMATION: Human teneurin
184 <400> SEQUENCE: 3

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Input Set : A:\1-32724 SEQLIST.TXT
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185 atg gat gta aag gac cg	cg	cac	cgc	tct	ttg	acc	aga	gga	cgc	tgt	48
186 Met Asp Val Lys Asp Arg	Arg	Arg	His	Arg	Ser	Leu	Thr	Arg	Gly	Arg	Cys
187 1	5				10				15		
189 ggc aaa gag tgt cgc tac aca agc tcc tct ctg gac agt gag gac tgc											96
190 Gly Lys Glu Cys Arg Tyr Thr Ser Ser Ser Leu Asp Ser Glu Asp Cys											
191 20		25				30					
193 cgc gtg ccc aca cag aaa tcc tac agc tcc agt gag act ctg aag gcc											144
194 Arg Val Pro Thr Gln Lys Ser Tyr Ser Ser Glu Thr Leu Lys Ala											
195 35		40				45					
197 tat gac cat gac agc agg atg cac tat gga aac cga gtc aca gac ctc											192
198 Tyr Asp His Asp Ser Arg Met His Tyr Gly Asn Arg Val Thr Asp Leu											
199 50		55			60						
201 atc cac cgg gag tca gat gag ttt cct aga caa gga acc aac ttc acc											240
202 Ile His Arg Glu Ser Asp Glu Phe Pro Arg Gln Gly Thr Asn Phe Thr											
203 65		70			75				80		
205 ctt gcc gaa ctg ggc atc tgt gag ccc tcc cca cac cga agc ggc tac											288
206 Leu Ala Glu Leu Gly Ile Cys Glu Pro Ser Pro His Arg Ser Gly Tyr											
207 85			90			95					
209 tgc tcc gac atg ggg atc ctt cac cag ggc tac tcc ctt agc aca ggg											336
210 Cys Ser Asp Met Gly Ile Leu His Gln Gly Tyr Ser Leu Ser Thr Gly											
211 100		105			110						
213 tct gac gcc gac tcc gac acc gag gga ggg atg tct cca gaa cac gcc											384
214 Ser Asp Ala Asp Ser Asp Thr Glu Gly Gly Met Ser Pro Glu His Ala											
215 115		120			125						
217 atc aga ctg tgg ggc aga ggg ata aaa tcc agg cgc agt tcc ggc ctg											432
218 Ile Arg Leu Trp Gly Arg Gly Ile Lys Ser Arg Arg Ser Ser Gly Leu											
219 130		135			140						
221 tcc agt cgt gaa aac tcg gcc ctt acc ctg act gac tct gac aac gaa											480
222 Ser Ser Arg Glu Asn Ser Ala Leu Thr Leu Thr Asp Ser Asp Asn Glu											
223 145		150			155				160		
225 aac aaa tca gat gat gag aac gaa agt cgt ccc att cca cct aca tcc											528
226 Asn Lys Ser Asp Asp Glu Asn Glu Ser Arg Pro Ile Pro Pro Thr Ser											
227 165			170			175					
229 tcg cct agt ctc ctc cca tct gct cag ctg cct agc tcc cat aat cct											576
230 Ser Pro Ser Leu Leu Pro Ser Ala Gln Leu Pro Ser Ser His Asn Pro											
231 180		185			190						
233 cca cca gtt agc tgc cag atg cca ttg cta gac agc aac acc tcc cat											624
234 Pro Pro Val Ser Cys Gln Met Pro Leu Leu Asp Ser Asn Thr Ser His											
235 195		200			205						
237 caa atc atg gac acc aac cct gat gag gaa ttc tcc ccc aat tca tac											672
238 Gln Ile Met Asp Thr Asn Pro Asp Glu Glu Phe Ser Pro Asn Ser Tyr											
239 210		215			220						
241 ctg ctc aga gca tgc tca ggg ccc cag caa gcc tcc agc agt ggc cct											720
242 Leu Leu Arg Ala Cys Ser Gly Pro Gln Gln Ala Ser Ser Ser Gly Pro											
243 225		230			235				240		
245 ccg aac cac cac agc cag tcg act ctg agg ccc cct ctc cca ccc cct											768
246 Pro Asn His His Ser Gln Ser Thr Leu Arg Pro Pro Leu Pro Pro Pro											
247 245			250			255					
249 cac aac cac acg ctg tcc cat cac cac tcg tcc gcc aac tcc ctc aac											816

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PATENT APPLICATION: US/10/530,542

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Input Set : A:\1-32724 SEQLIST.TXT
Output Set: N:\CRF4\11212005\J530542.raw

250	His	Asn	His	Thr	Leu	Ser	His	His	Ser	Ser	Ala	Asn	Ser	Leu	Asn		
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254	Arg	Asn	Ser	Leu	Thr	Asn	Arg	Arg	Ser	Gln	Ile	His	Ala	Pro	Ala	Pro	
255				275			280			285							
257	gcg	ccc	aat	gac	ctg	gcc	acc	aca	cca	gag	tcc	gtt	cag	ctt	cag	gac	912
258	Ala	Pro	Asn	Asp	Leu	Ala	Thr	Thr	Pro	Glu	Ser	Val	Gln	Leu	Gln	Asp	
259				290			295			300							
261	agc	tgg	gtg	cta	aac	agc	aac	gtg	cca	ctg	gag	acc	cg	cac	ttc	ctc	960
262	Ser	Trp	Val	Leu	Asn	Ser	Asn	Val	Pro	Leu	Glu	Thr	Arg	His	Phe	Leu	
263	305				310				315			320					
265	ttc	aag	acc	tcc	tcg	ggg	agc	aca	ccc	ttg	ttc	agc	agc	tct	tcc	ccg	1008
266	Phe	Lys	Thr	Ser	Ser	Gly	Ser	Thr	Pro	Leu	Phe	Ser	Ser	Ser	Ser	Pro	
267					325			330			335						
269	gga	tac	cct	ttg	acc	tca	gga	acg	gtt	tac	acg	ccc	ccg	ccc	cg	ctg	1056
270	Gly	Tyr	Pro	Leu	Thr	Ser	Gly	Thr	Val	Tyr	Thr	Pro	Pro	Pro	Arg	Leu	
271					340			345			350						
273	ctg	ccc	agg	aat	act	tcc	tcc	agg	aag	gct	ttc	aag	ctg	aag	aag	ccc	1104
274	Leu	Pro	Arg	Asn	Thr	Phe	Ser	Arg	Lys	Ala	Phe	Lys	Leu	Lys	Lys	Pro	
275					355			360			365						
277	tcc	aaa	tac	tgc	agc	tgg	aaa	tgt	gct	gcc	ctc	tcc	gcc	att	gcc	gcg	1152
278	Ser	Lys	Tyr	Cys	Ser	Trp	Lys	Cys	Ala	Ala	Leu	Ser	Ala	Ile	Ala	Ala	
279					370			375			380						
281	gcc	ctc	ctc	ttg	gct	att	ttg	ctg	gcg	tat	ttc	ata	gca	atg		1194	
282	Ala	Leu	Leu	Leu	Ala	Ile	Leu	Leu	Ala	Tyr	Phe	Ile	Ala	Met			
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287	<210>	SEQ	ID	NO:	4												
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294	1			5				10			15						
295	Gly	Lys	Glu	Cys	Arg	Tyr	Thr	Ser	Ser	Ser	Leu	Asp	Ser	Glu	Asp	Cys	
296				20				25			30						
297	Arg	Val	Pro	Thr	Gln	Lys	Ser	Tyr	Ser	Ser	Ser	Glu	Thr	Leu	Lys	Ala	
298					35			40			45						
299	Tyr	Asp	His	Asp	Ser	Arg	Met	His	Tyr	Gly	Asn	Arg	Val	Thr	Asp	Leu	
300					50			55			60						
301	Ile	His	Arg	Glu	Ser	Asp	Glu	Phe	Pro	Arg	Gln	Gly	Thr	Asn	Phe	Thr	
302	65				70				75			80					
303	Leu	Ala	Glu	Leu	Gly	Ile	Cys	Glu	Pro	Ser	Pro	His	Arg	Ser	Gly	Tyr	
304					85			90			95						
305	Cys	Ser	Asp	Met	Gly	Ile	Leu	His	Gln	Gly	Tyr	Ser	Leu	Ser	Thr	Gly	
306					100			105			110						
307	Ser	Asp	Ala	Asp	Ser	Asp	Thr	Glu	Gly	Gly	Met	Ser	Pro	Glu	His	Ala	
308					115			120			125						
309	Ile	Arg	Leu	Trp	Gly	Arg	Gly	Ile	Lys	Ser	Arg	Arg	Ser	Ser	Gly	Leu	
310					130			135			140						

VERIFICATION SUMMARY

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Input Set : A:\1-32724 SEQLIST.TXT

Output Set: N:\CRF4\11212005\J530542.raw

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L:672 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:676 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:687 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:691 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:702 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:706 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
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L:732 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:736 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
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L:752 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:15
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L:768 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
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